SEQUENCE LISTING

<110> Merck & Co., Inc.
Harvey, Diane Marie
Yang, Yi
Kohl, Nancy

<120> ISOLATED NUCLEIC ACID MOLECULE ENCODING A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES THEREOF

<130> 21023-PCT

<150> 60/387,403
<151> 2002-06-10

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1488
<212> DNA
<213> Human

<400> 1
atggcggagg aaggagccgt ggccgtctgc gtgcgagtgc ggccgctgaa cagcagagaa 60
gaatcacttg gagaaactgc ccaagtttac tggaaaactg acaataatgt catttatcaa 120
gttgatggaa gtaaatcctt caattttgat cgtgtctttc atggtaatga aactaccaaa 180
aatgtgtatg aagaaatagc agcaccaatc atcgattctg ccatacaagg ctacaatggt 240
actatatttg cctatggaca gactgcttca ggaaaaacat ataccatgat gggttcagaa 300
gatcatttgg gagttatacc cagggcaatt catgacattt tccaaaaaat taagaagttt 360
cctgataggg aatttctctt acgtgtatct tacatggaaa tatacaatga aaccattaca 420
gatttactct gtggcactca aaaaatgaaa cctttaatta ttcgagaaga tgtcaatagg 480
aatgtgtatg ttgctgatct cacagaagaa gttgtatata catcagaaat ggctttgaaa 540
tggattacaa agggagaaaa gagcaggcat tatggagaaa caaaaatgaa tcaaagaagc 600
agtcgttctc ataccatctt taggatgatt ttggaaagca gagagaaggg tgaaccttct 660
aattgtgaag gatctgttaa ggtatcccat ttgaatttgg ttgatcttgc aggcagtgaa 720
agagctgctc aaacaggcgc tgcaggtgtg cggctcaagg aaggctgtaa tataaatcga 780
agcttattta ttttgggaca agtgatcaag aaacttagtg atggacaagt tggtggtttc 840
ataaattatc gagatagcaa gttaacacga attctccaga attccttggg aggaaatgca 900
aagacacgta ttatctgcac aattactcca gtatcttttg atgaaacact tactgctctc 960
cagtttgcca gtactgctaa atatatgaag aatactcctt atgttaatga ggtatcaact 1020
gatgaagctc tcctgaaaag gtatagaaaa gaaataatgg atcttaaaaa acaattagag 1080
gaggtttctt tagagacgcg ggctcaggca atggaaaaag accaattggc ccaacttttg 1140
gaagaaaaag atttgcttca gaaagtacag aatgagaaaa ttgaaaactt aacacggatg 1200
ctggtgacct cttcttccct cacgttgcaa caggaattaa aggctaaaag aaaacgaaga 1260
gttacttggt gccttggcaa aattaacaaa atgaagaact caaactatgc agatcaattt 1320
aatataccaa caaatataac aacaaaaaca cataagcttt ctataaattt attacgagaa 1380
attgatgaat ctgtcggtac catatgggaa ttcgaagctt acgtagaaca aaaactcatc 1440
tcagaagagg atctgaatag cgccgtcgac catcatcatc atcatcat 1488

<210> 2
<211> 496
<212> PRT
<213> Human

<400> 2
Met Ala Glu Glu Gly Ala Val Ala Val Cys Val Arg Val Arg Pro Leu
1 5 10 15
Asn Ser Arg Glu Glu Ser Leu Gly Glu Thr Ala Gln Val Tyr Trp Lys

```
            20                  25                  30
Thr Asp Asn Asn Val Ile Tyr Gln Val Asp Gly Ser Lys Ser Phe Asn
        35                  40                  45
Phe Asp Arg Val Phe His Gly Asn Glu Thr Thr Lys Asn Val Tyr Glu
    50                  55                  60
Glu Ile Ala Ala Pro Ile Ile Asp Ser Ala Ile Gln Gly Tyr Asn Gly
65                  70                  75                  80
Thr Ile Phe Ala Tyr Gly Gln Thr Ala Ser Gly Lys Thr Tyr Thr Met
                85                  90                  95
Met Gly Ser Glu Asp His Leu Gly Val Ile Pro Arg Ala Ile His Asp
            100                 105                 110
Ile Phe Gln Lys Ile Lys Lys Phe Pro Asp Arg Glu Phe Leu Leu Arg
        115                 120                 125
Val Ser Tyr Met Glu Ile Tyr Asn Glu Thr Ile Thr Asp Leu Leu Cys
    130                 135                 140
Gly Thr Gln Lys Met Lys Pro Leu Ile Ile Arg Glu Asp Val Asn Arg
145                 150                 155                 160
Asn Val Tyr Val Ala Asp Leu Thr Glu Glu Val Val Tyr Thr Ser Glu
                165                 170                 175
Met Ala Leu Lys Trp Ile Thr Lys Gly Glu Lys Ser Arg His Tyr Gly
            180                 185                 190
Glu Thr Lys Met Asn Gln Arg Ser Ser Arg Ser His Thr Ile Phe Arg
        195                 200                 205
Met Ile Leu Glu Ser Arg Glu Lys Gly Glu Pro Ser Asn Cys Glu Gly
    210                 215                 220
Ser Val Lys Val Ser His Leu Asn Leu Val Asp Leu Ala Gly Ser Glu
225                 230                 235                 240
Arg Ala Ala Gln Thr Gly Ala Ala Gly Val Arg Leu Lys Glu Gly Cys
                245                 250                 255
Asn Ile Asn Arg Ser Leu Phe Ile Leu Gly Gln Val Ile Lys Lys Leu
            260                 265                 270
Ser Asp Gly Gln Val Gly Gly Phe Ile Asn Tyr Arg Asp Ser Lys Leu
        275                 280                 285
Thr Arg Ile Leu Gln Asn Ser Leu Gly Gly Asn Ala Lys Thr Arg Ile
    290                 295                 300
Ile Cys Thr Ile Thr Pro Val Ser Phe Asp Glu Thr Leu Thr Ala Leu
305                 310                 315                 320
Gln Phe Ala Ser Thr Ala Lys Tyr Met Lys Asn Thr Pro Tyr Val Asn
                325                 330                 335
Glu Val Ser Thr Asp Glu Ala Leu Leu Lys Arg Tyr Arg Lys Glu Ile
            340                 345                 350
Met Asp Leu Lys Lys Gln Leu Glu Glu Val Ser Leu Glu Thr Arg Ala
        355                 360                 365
Gln Ala Met Glu Lys Asp Gln Leu Ala Gln Leu Leu Glu Glu Lys Asp
    370                 375                 380
Leu Leu Gln Lys Val Gln Asn Glu Lys Ile Glu Asn Leu Thr Arg Met
385                 390                 395                 400
Leu Val Thr Ser Ser Ser Leu Thr Leu Gln Gln Glu Leu Lys Ala Lys
                405                 410                 415
Arg Lys Arg Arg Val Thr Trp Cys Leu Gly Lys Ile Asn Lys Met Lys
            420                 425                 430
Asn Ser Asn Tyr Ala Asp Gln Phe Asn Ile Pro Thr Asn Ile Thr Thr
        435                 440                 445
Lys Thr His Lys Leu Ser Ile Asn Leu Leu Arg Glu Ile Asp Glu Ser
    450                 455                 460
Val Gly Thr Ile Trp Glu Phe Glu Ala Tyr Val Glu Gln Lys Leu Ile
465                 470                 475                 480
Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His His His
                485                 490                 495
```

<210> 3

<211> 1065
<212> DNA
<213> Human

<400> 3
atggcggagg aaggagccgt ggccgtctgc gtgcgagtgc ggccgctgaa cagcagagaa 60
gaatcacttg gagaaactgc ccaagtttac tggaaaactg acaataatgt catttatcaa 120
gttgatggaa gtaaatcctt caattttgat cgtgtctttc atggtaatga aactaccaaa 180
aatgtgtatg aagaaatagc agcaccaatc atcgattctg ccatacaagg ctacaatggt 240
actatatttg cctatggaca gactgcttca ggaaaaacat ataccatgat gggttcagaa 300
gatcatttgg gagttatacc cagggcaatt catgacattt tccaaaaaat taagaagttt 360
cctgataggg aatttctctt acgtgtatct tacatggaaa tatacaatga aaccattaca 420
gatttactct gtggcactca aaaaatgaaa cctttaatta ttcgagaaga tgtcaatagg 480
aatgtgtatg ttgctgatct cacagaagaa gttgtatata catcagaaat ggctttgaaa 540
tggattacaa agggagaaaa gagcaggcat tatggagaaa caaaaatgaa tcaaagaagc 600
agtcgttctc ataccatctt taggatgatt ttggaaagca gagagaaggg tgaaccttct 660
aattgtgaag gatctgttaa ggtatcccat ttgaatttgg ttgatcttgc aggcagtgaa 720
agagctgctc aaacaggcgc tgcaggtgtg cggctcaagg aaggctgtaa tataaatcga 780
agcttattta ttttgggaca agtgatcaag aaacttagtg atggacaagt tggtggtttc 840
ataaattatc gagatagcaa gttaacacga attctccaga attccttggg aggaaatgca 900
aagacacgta ttatctgcac aattactcca gtatcttttg atgaaacact tactgctctc 960
cagtttgcca gtactgctaa atatatgaag aatactcctt atgttaatga ggtatcaact 1020
gtcgacaagc ttgcggccgc actcgagcac caccaccacc accac 1065

<210> 4
<211> 355
<212> PRT
<213> Human

<400> 4
Met Ala Glu Glu Gly Ala Val Ala Val Cys Val Arg Val Arg Pro Leu
1 5 10 15
Asn Ser Arg Glu Glu Ser Leu Gly Glu Thr Ala Gln Val Tyr Trp Lys
20 25 30
Thr Asp Asn Asn Val Ile Tyr Gln Val Asp Gly Ser Lys Ser Phe Asn
35 40 45
Phe Asp Arg Val Phe His Gly Asn Glu Thr Thr Lys Asn Val Tyr Glu
50 55 60
Glu Ile Ala Ala Pro Ile Ile Asp Ser Ala Ile Gln Gly Tyr Asn Gly
65 70 75 80
Thr Ile Phe Ala Tyr Gly Gln Thr Ala Ser Gly Lys Thr Tyr Thr Met
85 90 95
Met Gly Ser Glu Asp His Leu Gly Val Ile Pro Arg Ala Ile His Asp
100 105 110
Ile Phe Gln Lys Ile Lys Lys Phe Pro Asp Arg Glu Phe Leu Leu Arg
115 120 125
Val Ser Tyr Met Glu Ile Tyr Asn Glu Thr Ile Thr Asp Leu Leu Cys
130 135 140
Gly Thr Gln Lys Met Lys Pro Leu Ile Ile Arg Glu Asp Val Asn Arg
145 150 155 160
Asn Val Tyr Val Ala Asp Leu Thr Glu Glu Val Val Tyr Thr Ser Glu
165 170 175
Met Ala Leu Lys Trp Ile Thr Lys Gly Glu Lys Ser Arg His Tyr Gly
180 185 190
Glu Thr Lys Met Asn Gln Arg Ser Ser Arg Ser His Thr Ile Phe Arg
195 200 205
Met Ile Leu Glu Ser Arg Glu Lys Gly Glu Pro Ser Asn Cys Glu Gly
210 215 220
Ser Val Lys Val Ser His Leu Asn Leu Val Asp Leu Ala Gly Ser Glu
225 230 235 240
Arg Ala Ala Gln Thr Gly Ala Ala Gly Val Arg Leu Lys Glu Gly Cys
245 250 255

```
Asn Ile Asn Arg Ser Leu Phe Ile Leu Gly Gln Val Ile Lys Lys Leu
                260                 265                 270
Ser Asp Gly Gln Val Gly Gly Phe Ile Asn Tyr Arg Asp Ser Lys Leu
            275                 280                 285
Thr Arg Ile Leu Gln Asn Ser Leu Gly Gly Asn Ala Lys Thr Arg Ile
    290                 295                 300
Ile Cys Thr Ile Thr Pro Val Ser Phe Asp Glu Thr Leu Thr Ala Leu
305                 310                 315                 320
Gln Phe Ala Ser Thr Ala Lys Tyr Met Lys Asn Thr Pro Tyr Val Asn
                325                 330                 335
Glu Val Ser Thr Val Asp Lys Leu Ala Ala Ala Leu Glu His His His
            340                 345                 350
His His His
        355
```